Fig. 1

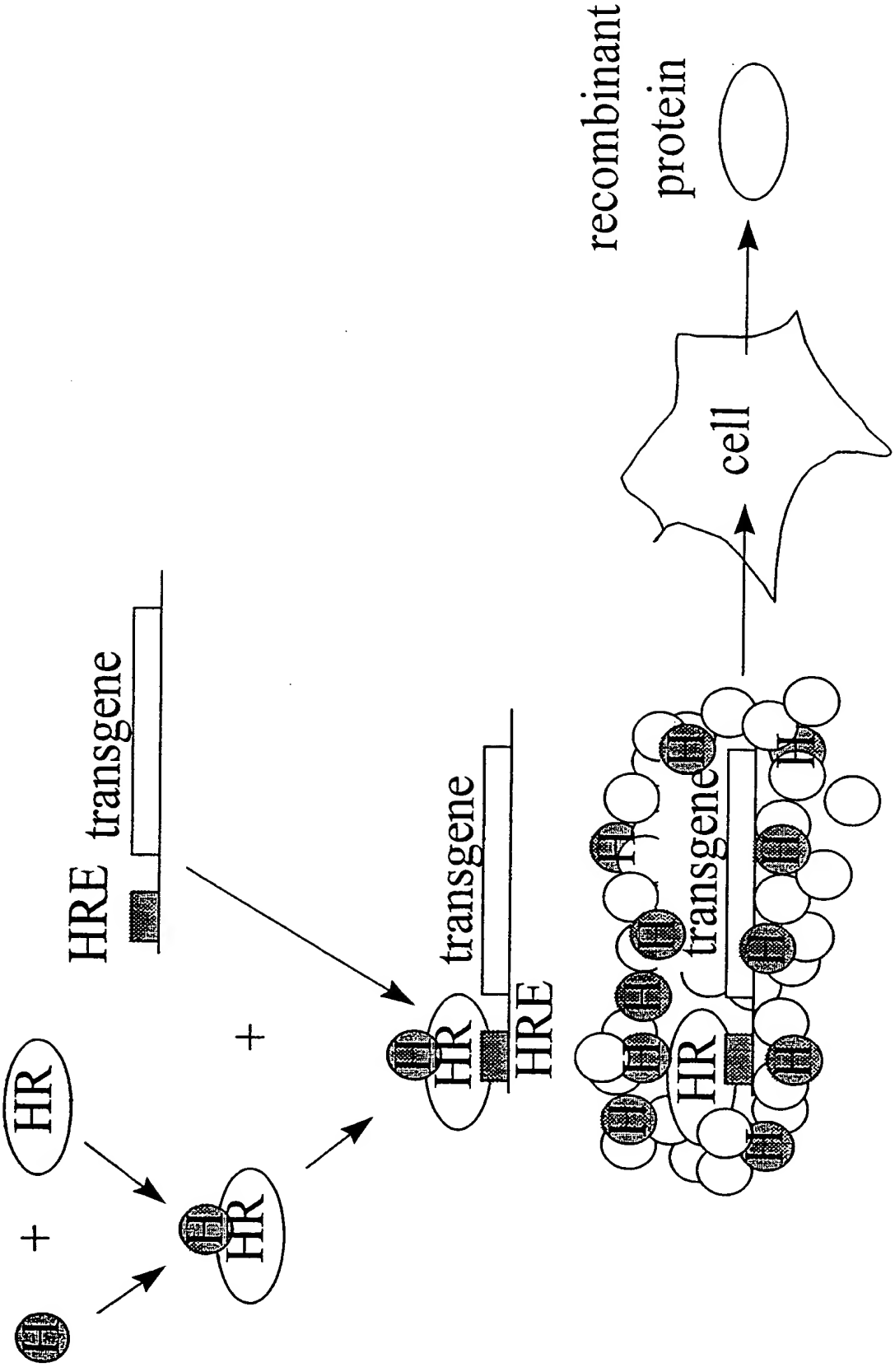

HR
HR
HRE
transgene
HR
HRE
transgene
HR
transgene
cell
recombinant
protein

Fig. 2

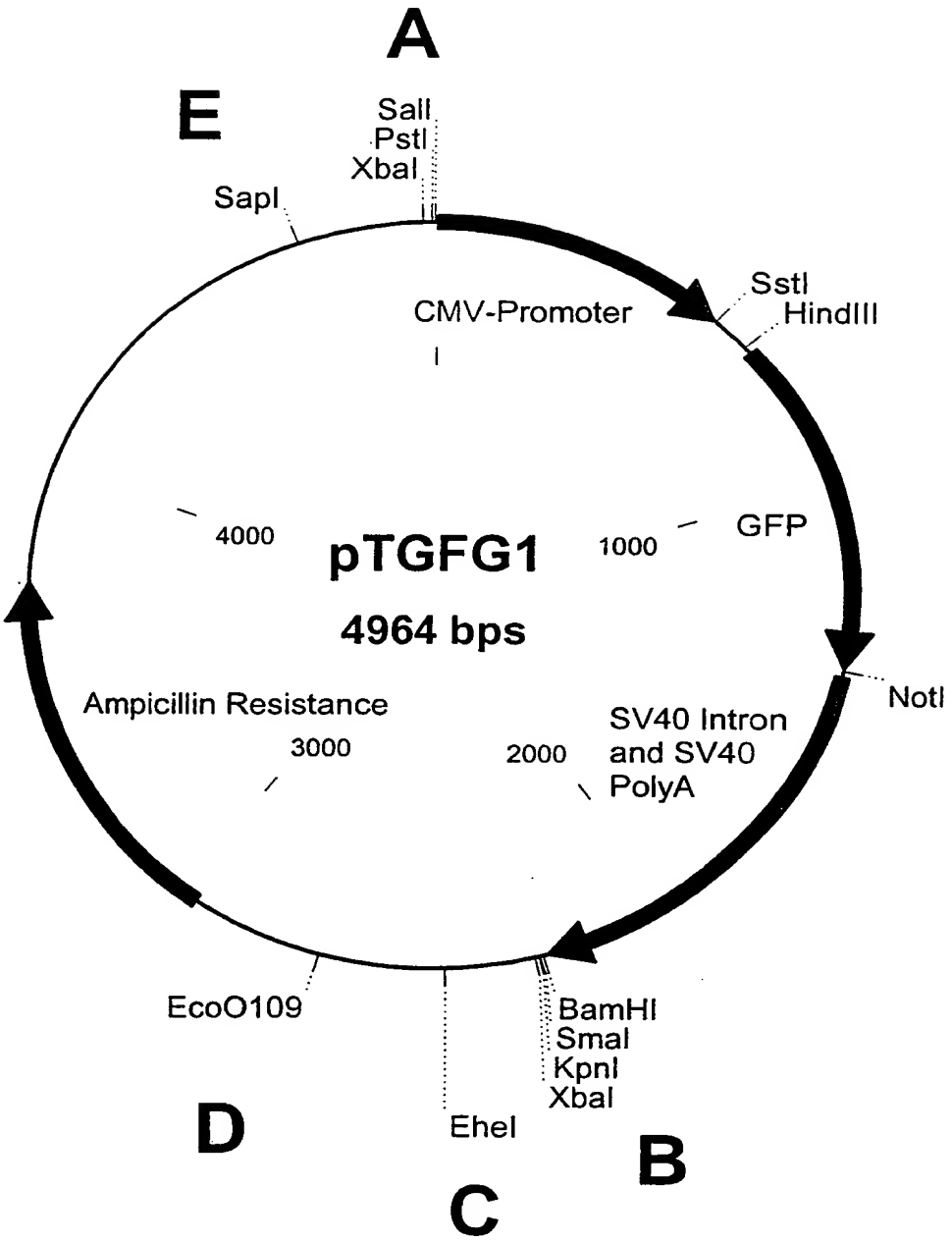
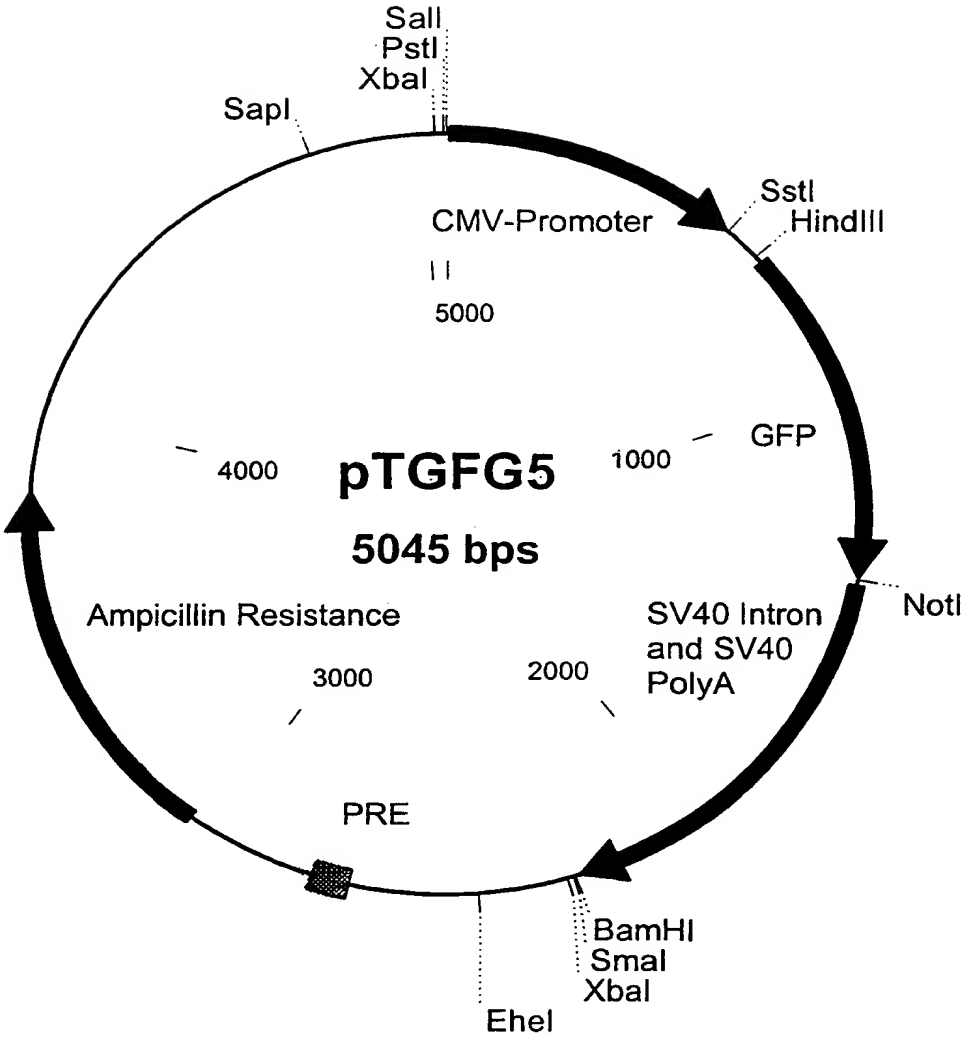

A
B
C
D
E
SalI
PstI
XbaI
SapI
SstI
HindIII
CMV-Promoter
GFP
1000
pTGFG1
4964 bps
4000
NotI
Ampicillin Resistance
3000
SV40 Intron
and SV40
PolyA
2000
EcoO109
BamHI
SmaI
KpnI
XbaI
EheI

Fig. 3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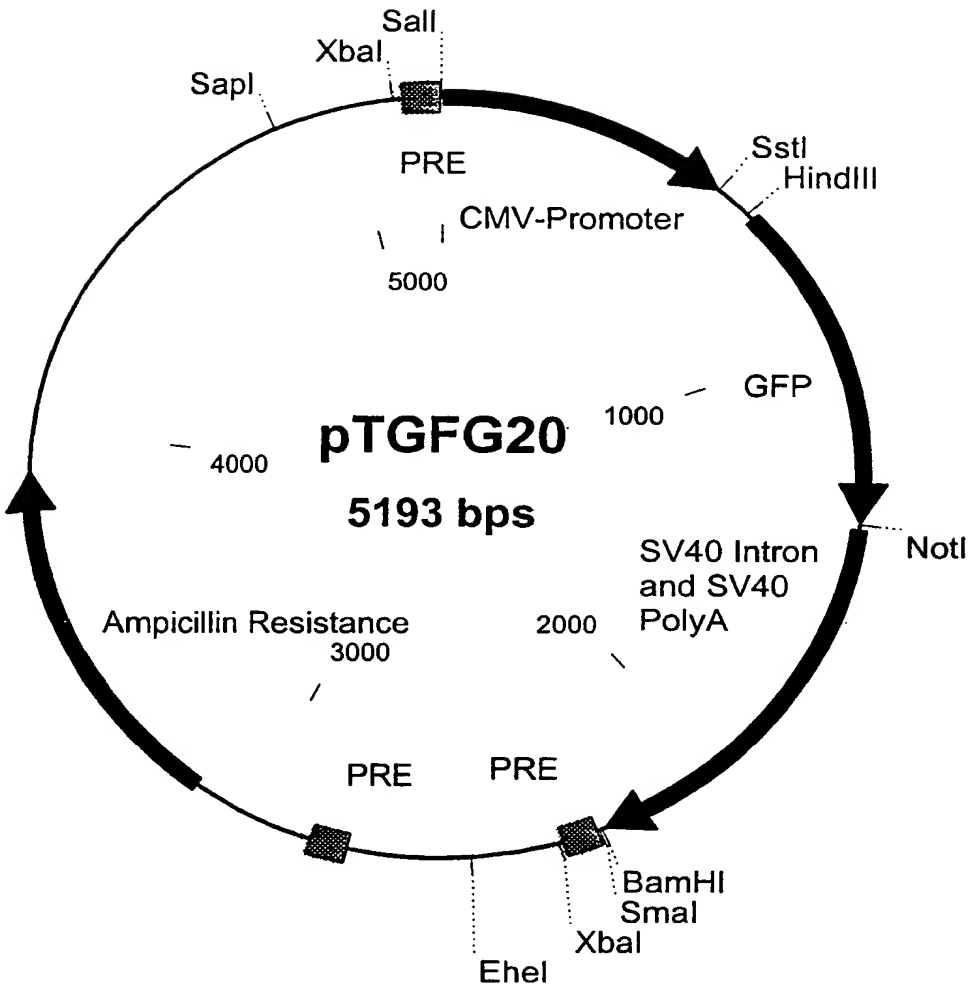
PstI
XbaI
SapI
SstI
HindIII
CMV-Promoter
5000
GFP
1000
pTGFG5
5045 bps
4000
Ampicillin Resistance
3000
2000
SV40 Intron
and SV40
PolyA
NotI
PRE
BamHI
SmaI
XbaI
EheI

Fig. 4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XbaI
SapI
PRE
SstI
HindIII
CMV-Promoter
5000
GFP
1000
pTGFG20
5193 bps
4000
SV40 Intron
and SV40
PolyA
NotI
2000
Ampicillin Resistance
3000
PRE
PRE
BamHI
SmaI
XbaI
EheI

Fig. 5

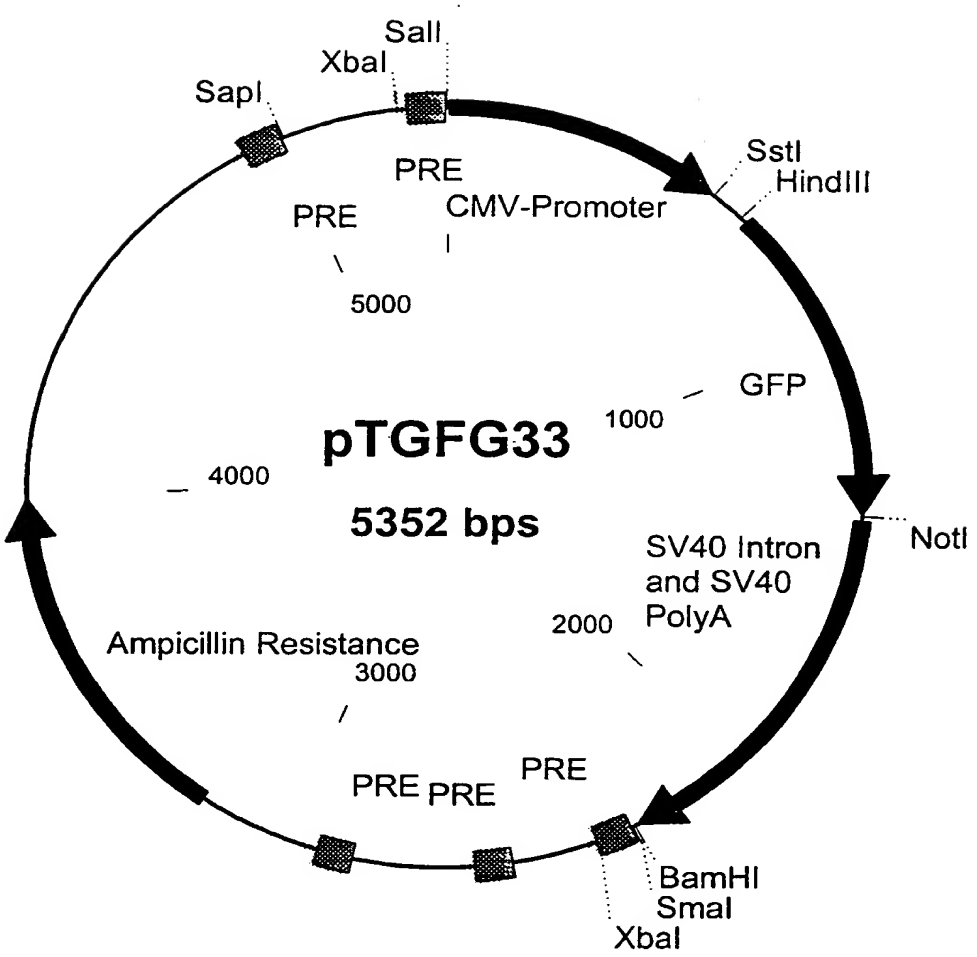

SalI
XbaI
SapI
PRE
PRE
CMV-Promoter
SstI
HindIII
5000
GFP
1000
pTGFG33
5352 bps
4000
NotI
SV40 Intron
and SV40
PolyA
2000
Ampicillin Resistance
3000
PRE
PRE
PRE
BamHI
SmaI
XbaI

Fig. 6

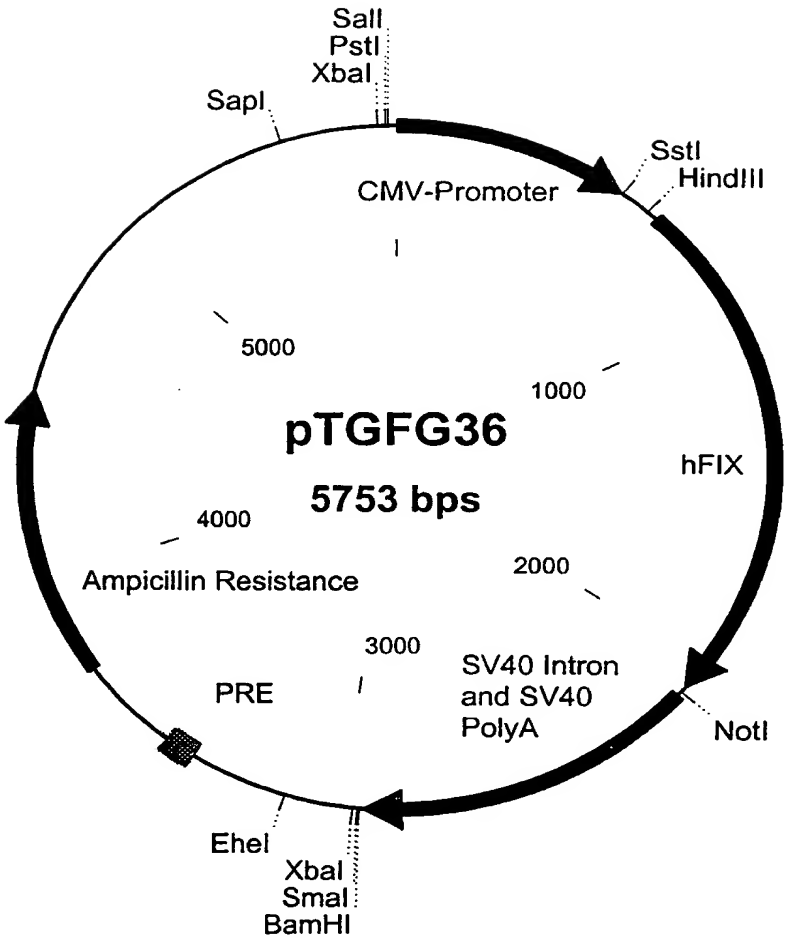

SalI
PstI
XbaI
SapI
SstI
HindIII
CMV-Promoter
1000
hFIX
2000
NotI
SV40 Intron
and SV40
PolyA
3000
PRE
EheI
XbaI
SmaI
BamHI
4000
Ampicillin Resistance
5000
pTGFG36
5753 bps

Fig. 7

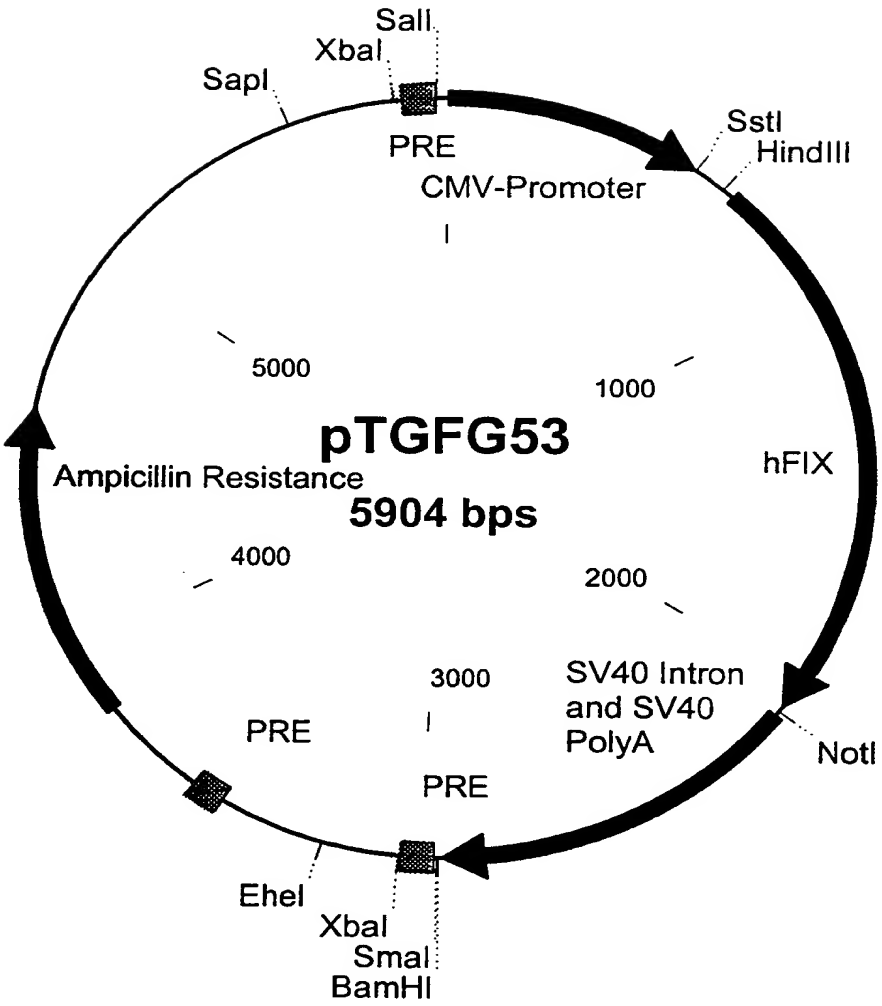
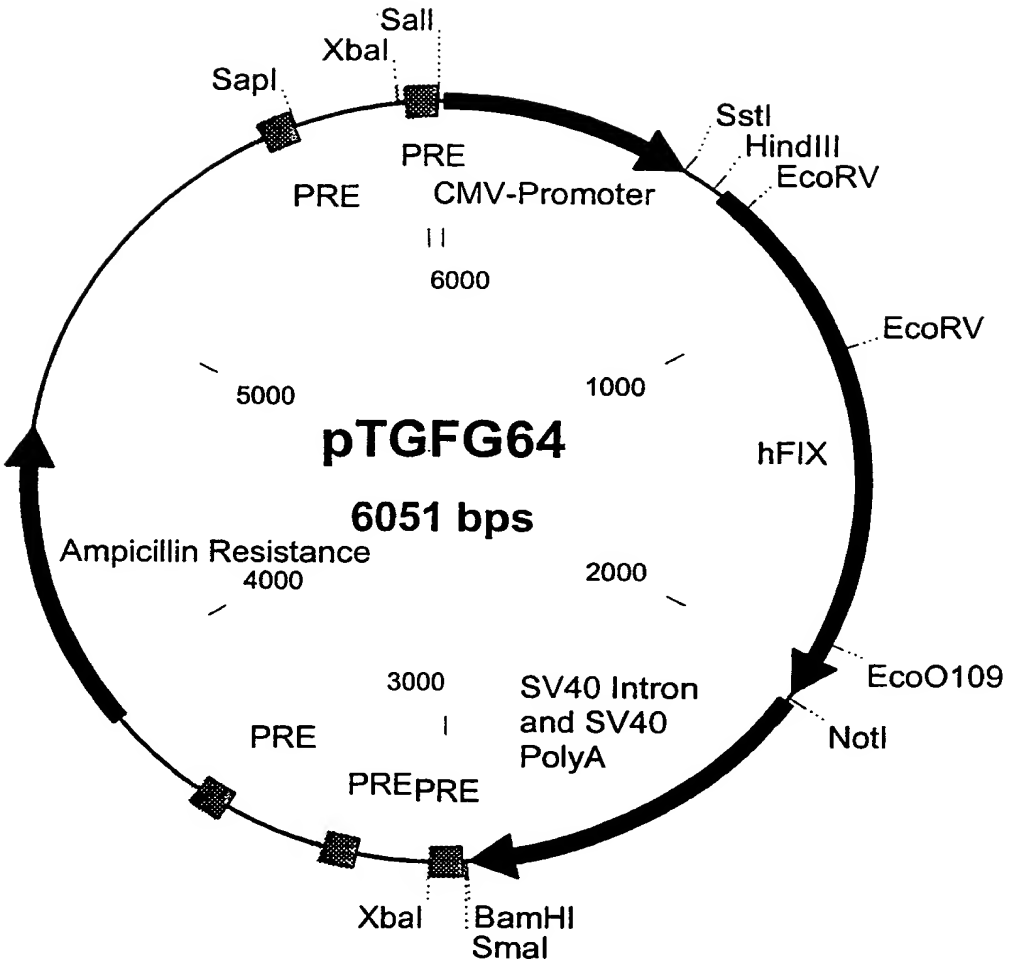

SalI
XbaI
SapI
PRE
CMV-Promoter
SstI
HindIII
1000
hFIX
2000
SV40 Intron
and SV40
PolyA
NotI
3000
PRE
PRE
PRE
EheI
XbaI
SmaI
BamHI
4000
5000
pTGFG53
Ampicillin Resistance
5904 bps

Fig. 8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XbaI
SapI
SstI
HindIII
EcoRV
PRE
PRE
CMV-Promoter
6000
EcoRV
1000
5000
pTGFG64
hFIX
6051 bps
Ampicillin Resistance
4000
2000
EcoO109
3000
SV40 Intron
and SV40
PolyA
NotI
PRE
PREPRE
XbaI
BamHI
SmaI

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Fig. 9

CGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTC
CGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTA
TGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAG
TACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAG
TACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTG
GCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTT
TGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGT
GTACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATAC
GACTCACTATAGGGAGACCCAAGCTTGCATGCCAATTCCGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAATC
ACCAGGCCTCATCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTTGATCATGAAAACGCCA
ACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGT
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TGTTGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTT
GGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGCAGTTT
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ACCAGCAGTGCCATTTCCATGTGGAAGAGTTTCTGTTTCACAAACTTCTAAGCTCACCCGTGCTGAGACTGTTTTTCCTG
ATGTGGACTATGTAAATTCTACTGAAGCTGAAACCATTTTGGATAACATCACTCAAAGCACCCAATCATTTAATGACTTC
ACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAATTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATT
CTGTGGAGGCTCTATCGTTAATGAAAAATGGATTGTAACTGCTGCCCACTGTGTTGAAACTGGTGTTAAAATTACAGTTG
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TACAATGCAGCTATTAATAAGTACAACCATGACATTGCCCTTCTGGAACTGGACGAACCCTTAGTGCTAAACAGCTACGT
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AAGGCAAATATGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAAAAACAAAGCTCACTTAATGGGAT
CGGTCGAGCGGCCGCGACTCTACTAGAGGATCTTTGTGAAGGAACCTTACTTCTGTGGTGTGACATAATTGGACAAACTA
CCTACAGAGATTTAAAGCTCTAAGGTAAATATAAAATTTTTAAGTGTATAATGTGTTAAACTACTGATTCTAATTGTTTG
TGTATTTTAGATTCCAACCTATGGAACTGATGAATGGGAGCAGTGGTGGAATGCCTTTAATGAGGAAAACCTGTTTTGCT
CAGAAGAAATGCCATCTAGTGATGATGAGGCTACTGCTGACTCTCAACATTCTACTCCTCCAAAAAAGAAGAGAAAGGTA
GAAGACCCCAAGGACTTTCCTTCAGAATTGCTAAGTTTTTTGAGTCATGCTGTGTTTAGTAATAGAACTCTTGCTTGCTT
TGCTATTTACACCACAAAGGAAAAAGCTGCACTGCTATACAAGAAAATTATGGAAAAATATTCTGTAACCTTTATAAGTA
GGCATAACAGTTATAATCATAACATACTGTTTTTTCTTACTCCACACAGGCATAGAGTGTCTGCTATTAATAACTATGCT
CAAAAATTGTGTACCTTTAGCTTTTTAATTTGTAAAGGGGTTAATAAGGAATATTTGATGTATAGTGCCTTGACTAGAGA
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CACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGATCC
CCGGGTACCCTCTAGAGCGAATTAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAA
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GGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCC
TGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTC
ACCGTCATCACCGAAACGCGCGAGACGAAAGGGGGGGTACCAGCTTCGTAGCTAGAACATCATGTTCTGGGATATCAGCT
TCGTAGCTAGAACATCATGTTCTGGTACCCCCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTT
TCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATAT
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GTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGAT
GCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCC
CGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAG
AGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGAT
GGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGAT
CGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGC
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GGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCG
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TGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGA
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TTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTG
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TGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAA
GGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACT
CTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACC
GGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTT
GGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGG

Fig. 9 (continued)

CGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTT
TATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAA
AAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCC
CTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAG
TCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTG
GCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCC
AGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTAT
GACCATGATTACGCCAAGCTCTCTAGAGCTCTAGAGCTCTAGAGCTCTAGAGAGCTTGCATGCCTGCAGGTCG

Fig. 10

```
Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
 1               5                  10                  15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
            20                  25                  30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
        35                  40                  45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
    50                  55                  60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65                  70                  75                  80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
                85                  90                  95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
            100                 105                 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
        115                 120                 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
    130                 135                 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
145                 150                 155                 160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
                165                 170                 175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
            180                 185                 190

Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu
        195                 200                 205

Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
    210                 215                 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
225                 230                 235                 240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
                245                 250                 255

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
            260                 265                 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
        275                 280                 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn
    290                 295                 300
```

Fig. 10 (continued)

Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu
305 310 315 320

Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile
325 330 335

Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr
340 345 350

Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val
355 360 365

Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg
370 375 380

Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His
385 390 395 400

Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val
405 410 415

Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
420 425 430

Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
435 440 445

Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
450 455 460

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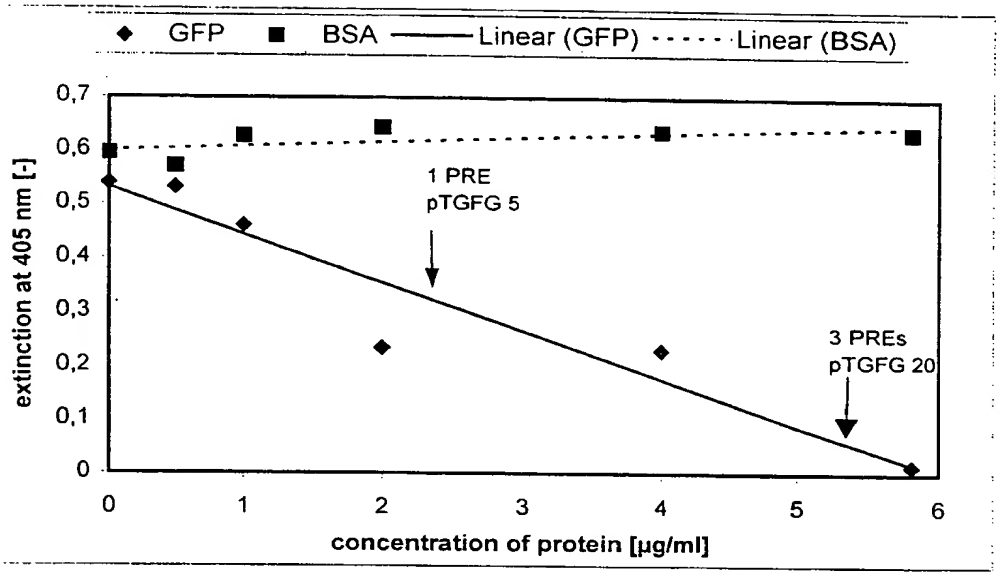
Fig. 11


GFP
BSA
Linear (GFP)
Linear (BSA)
extinction at 405 nm [-]
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
1 PRE
pTGFG 5
3 PREs
pTGFG 20
0
1
2
3
4
5
6
concentration of protein [µg/ml]

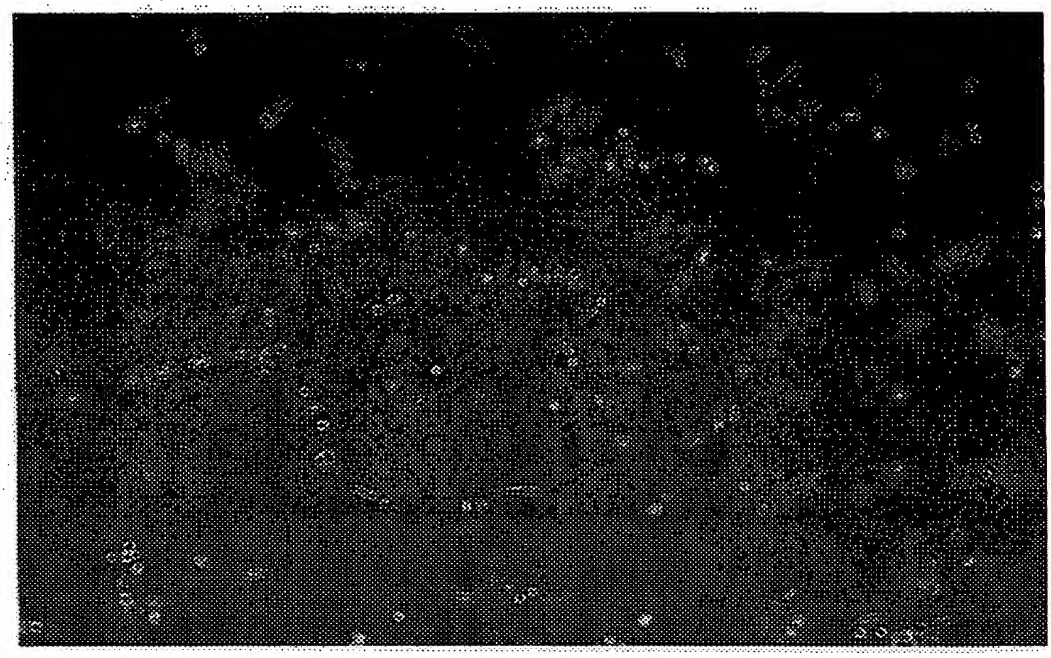


Fig. 12a

Fig 12 b

Fig 12 c

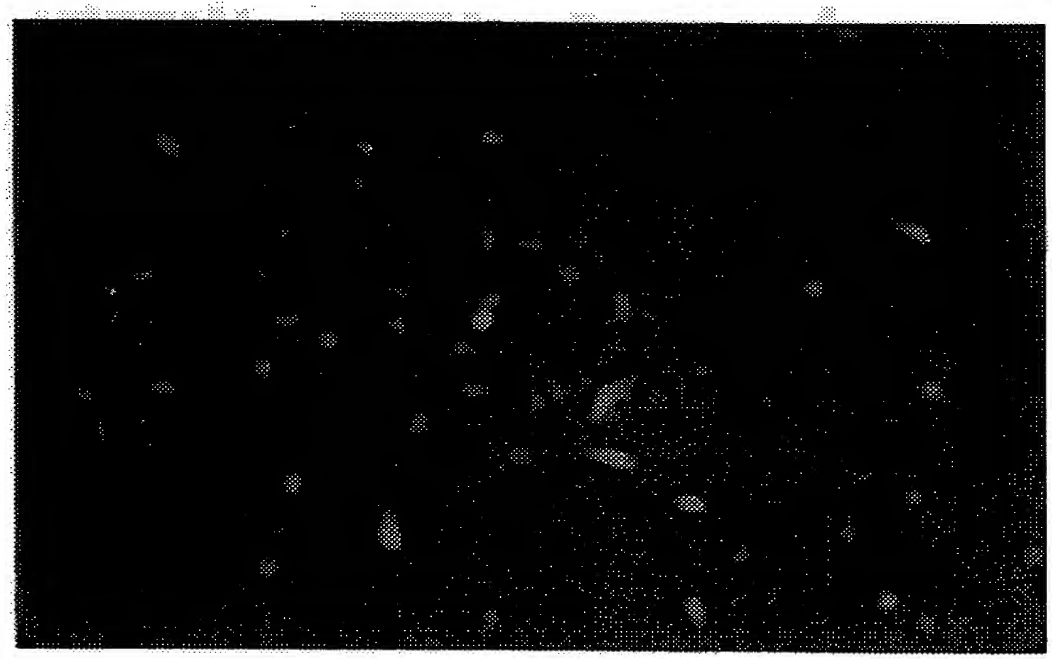


Fig 12 d

Fig. 13

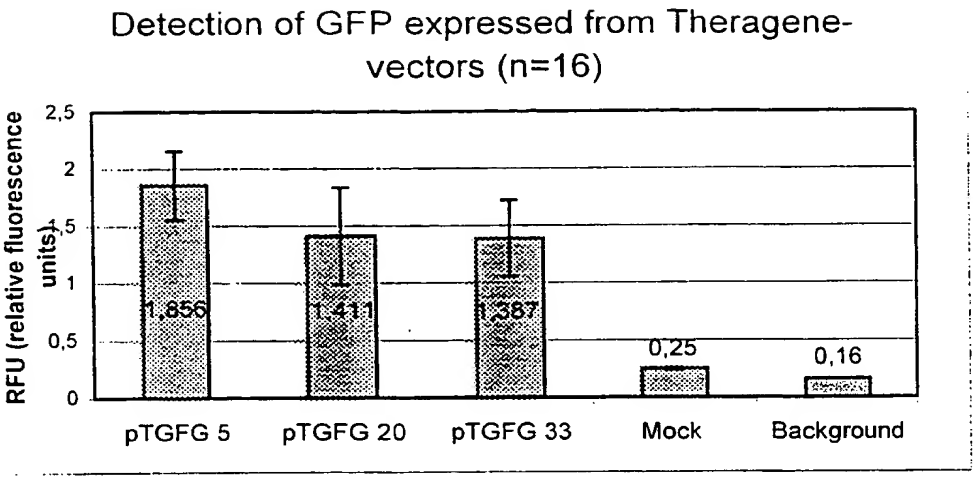


Fig. 14

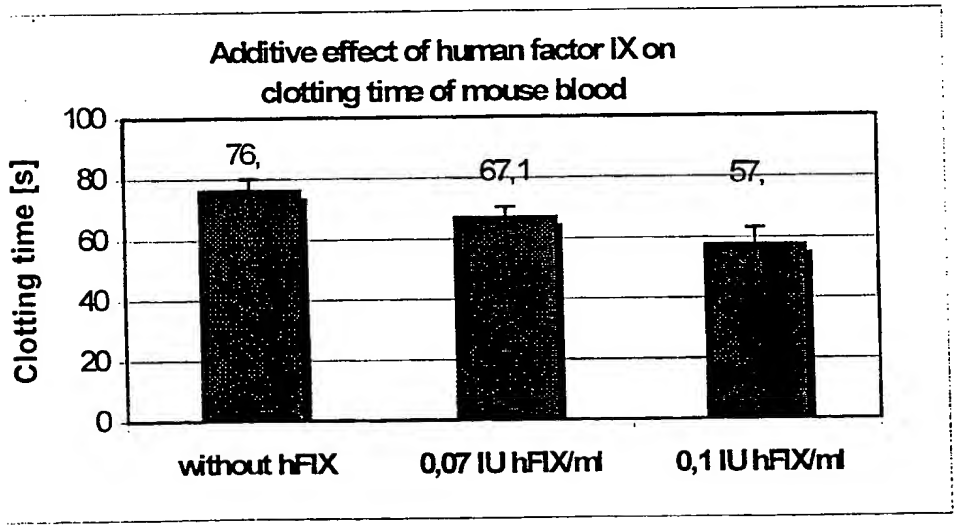


Fig. 15

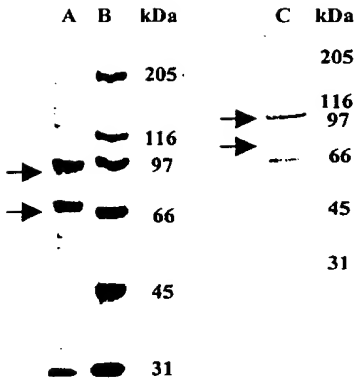
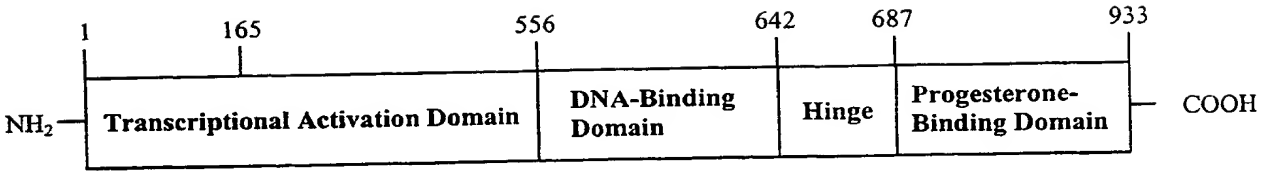


Fig. 16


1
165
556
642
687
933
NH2
Transcriptional Activation Domain
DNA-Binding Domain
Hinge
Progesterone-Binding Domain
COOH

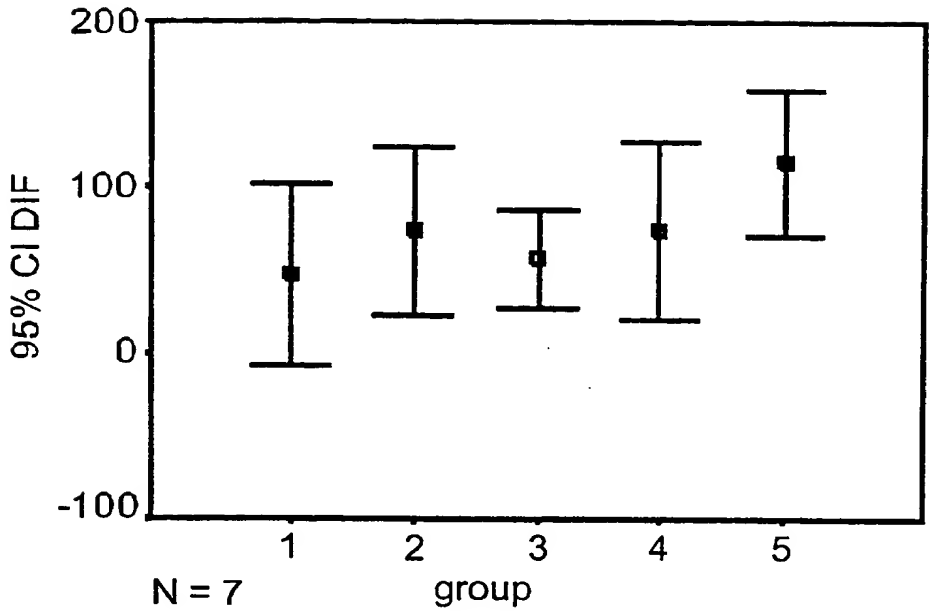

200
100
0
-100
95% CI DIF
1
2
3
4
5
N = 7
group

Fig. 17

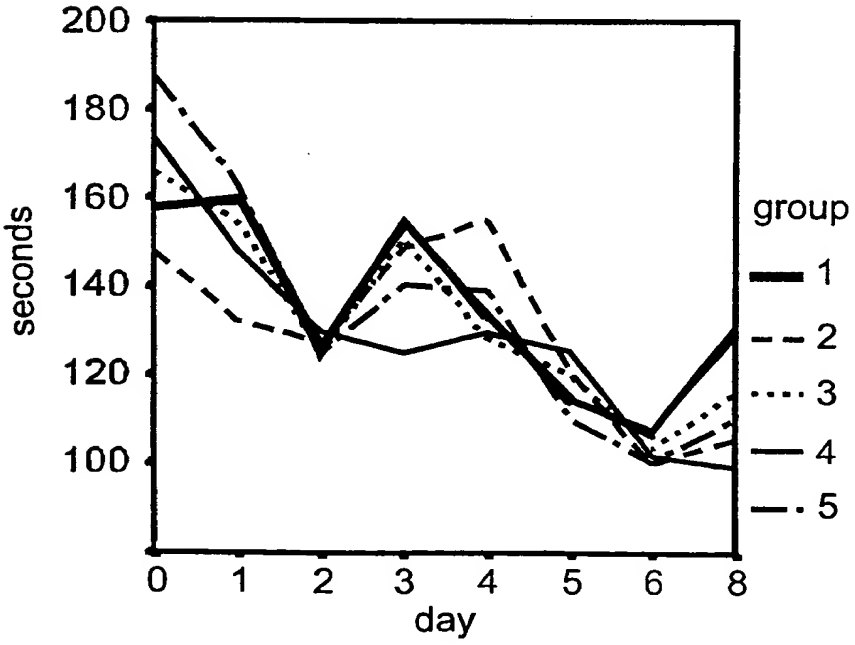
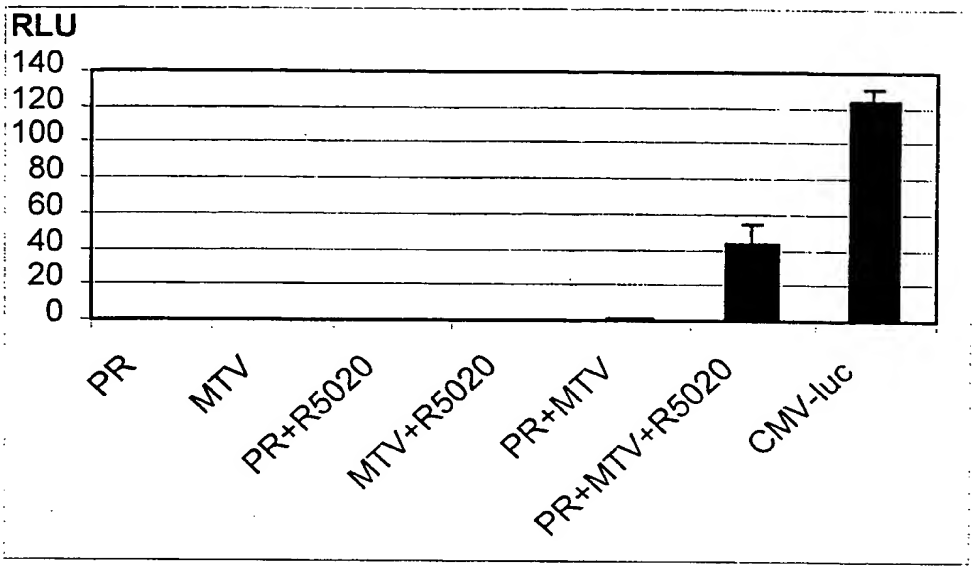

200
180
160
140
120
100
seconds
0
1
2
3
4
5
6
8
day
group
1
2
3
4
5

Fig. 18

Fig. 19


RLU
140
120
100
80
60
40
20
0
PR
MTV
PR+R5020
MTV+R5020
PR+MTV
PR+MTV+R5020
CMV-luc

```
1   MTELKAKGPR APHVAGGPPS PEVGSPLLCR PAAGPFPGSQ TSDTLPEVSA IPISLDGLLF
61  PRPCQGQDPS DEKTQDQQSL SDVEGAYSRA EATRGAGGSS SSPPEKDSGL LDSVLDTLLA
121 PSGPGQSQPS PPACEVTSSW CLFGPELPED PPAAPATQRV LSPLMSRSGC KVGDSSGTAA
181 AHKVLPRGLS PARQLLLPAS ESPHWSGAPV KPSPQAAAVE VEEEDGSESE ESAGPLLKGK
241 PRALGGAAAG GGAAAVPPGA AAGGVALVPK EDSRFSAPRV ALVEQDAPMA PGRSPLATTV
301 MDFIHVPILP LNHALLAART RQLLEDESYD GGAGAASAFA PPRSSPCASS TPVAVGDFPD
361 CAYPPDAEPK DDAYPLYSDF QPPALKIKEE EEGAEASARS PRSYLVAGAN PAAFPDFPLG
421 PPPPLPPRAT PSRPGEAAVT AAPASASVSS ASSSGSTLEC ILYKAEGAPP QQGPFAPPPC
481 KAPGASGCLL PRDGLPSTSA SAAAAGAAPA LYPALGLNGL PQLGYQAAVL KEGLPQVYPP
541 YLNYLRPDSE ASQSPQYSFE SLPQKICLIC GDEASGCHYG VLTCGSCKVF FKRAMEGQHN
601 YLCAGRNDCI VDKIRRKNCP ACRLRKCCQA GMVLGGRKFK KFNKVRVVRA LDAVALPQPL
661 GVPNESQALS QRFTFSPGQD IQLIPPLINL LMSIEPDVIY AGHDNTKPDT SSSLLTSLNQ
721 LGERQLLSVV KWSKSLPGFR NLHIDDQITL IQYSWMSLMV FGLGWRSYKH VSGQMLYFAP
781 DLILNEQRMK ESSFYSLCLT MWQIPQEFVK LQVSQEEFLC MKVLLLLNTI PLEGLRSQTQ
841 FEEMRSSYIR ELIKAIGLRQ KGVVSSSQRF YQLTKLLDNL HDLVKQLHLY CLNTFIQSRA
901 LSVEFPEMMS EVIAAQLPKI LAGMVKPLLF HKK
```

Fig. 20

```
1  ctgaccagcg ccgccctccc ccgcccccga cccaggaggt ggagatccct ccggtccagc
 61  cacattcaac acccactttc tcctccctct gcccctatat tcccgaaacc ccctcctcct
121  tccctttttcc ctcctccctg gagacggggg aggagaaaag gggagtccag tcgtcatgac
181  tgagctgaag gcaaagggtc cccgggctcc ccacgtggcg ggcggcccgc cctcccccga
241  ggtcggatcc ccactgctgt gtcgcccagc cgcaggtccg ttcccgggga gccagacctc
301  ggacaccttg cctgaagttt cggccatacc tatctccctg gacgggctac tcttccctcg
361  gccctgccag ggacaggacc cctccgacga aaagacgcag gaccagcagt cgctgtcgga
421  cgtggagggc gcatattcca gagctgaagc tacaaggggt gctggaggca gcagttctag
481  tcccccagaa aaggacagcg gactgctgga cagtgtcttg gacactctgt tggcgccctc
541  aggtcccggg cagagccaac ccagccctcc cgcctgcgag gtcaccagct cttggtgcct
601  gtttggcccc gaacttcccg aagatccacc ggctgccccc gccacccagc gggtgttgtc
661  cccgctcatg agccggtccg ggtgcaaggt tggagacagc tccgggacgg cagctgccca
721  taaagtgctg ccccggggcc tgtcaccagc ccggcagctg ctgctcccgg cctctgagag
781  ccctcactgg tccggggccc cagtgaagcc gtctccgcag gccgctgcgg tggaggttga
841  ggaggaggat ggctctgagt ccgaggagtc tgcgggtccg cttctgaagg gcaaacctcg
901  ggctctgggt ggcgcggcgg ctggaggagg agccgcggct gtcccgccgg gggcggcagc
961  aggaggcgtc gccctggtcc ccaaggaaga ttcccgcttc tcagcgccca gggtcgccct
1021 ggtggagcag gacgcgccga tggcgcccgg gcgctccccg ctggccacca cggtgatgga
1081 tttcatccac gtgcctatcc tgcctctcaa tcacgcctta ttggcagccc gcactcggca
1141 gctgctggaa gacgaaagtt acgacggcgg ggccggggct gccagcgcct ttgccccgcc
1201 gcggagttca ccctgtgcct cgtccacccc ggtcgctgta ggcgacttcc ccgactgcgc
1261 gtacccgccc gacgccgagc ccaaggacga cgcgtaccct ctctatagcg acttccagcc
1321 gcccgctcta aagataaagg aggaggagga aggcgcggag gcctccgcgc gctccccgcg
1381 ttcctacctt gtggccggtg ccaaccccgc agccttcccg gatttcccgt tggggccacc
1441 gcccccgctg ccgccgcgag cgaccccatc cagacccggg gaagcggcgg tgacggccgc
1501 acccgccagt gcctcagtct cgtctgcgtc ctcctcgggg tcgaccctgg agtgcatcct
1561 gtacaaagcg gagggcgcgc cgccccagca gggcccgttc gcgccgccgc cctgcaaggc
1621 gccgggcgcg agcggctgcc tgctcccgcg ggacggcctg ccctccacct ccgcctctgc
1681 cgccgccgcc ggggcggccc ccgcgctcta ccctgcactc ggcctcaacg ggctcccgca
1741 gctcggctac caggccgccg tgctcaagga gggcctgccg caggtctacc cgccctatct
1801 caactacctg aggccggatt cagaagccag ccagagccca caatacagct tcgagtcatt
1861 acctcagaag atttgtttaa tctgtgggga tgaagcatca ggctgtcatt atggtgtcct
1921 tacctgtggg agctgtaagg tcttctttaa gagggcaatg gaagggcagc acaactactt
1981 atgtgctgga agaaatgact gcatcgttga taaaatccgc agaaaaaact gcccagcatg
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2161 tccaaatgaa agccaagccc taagccagag attcactttt tcaccaggtc aagacataca
2221 gttgattcca ccactgatca acctgttaat gagcattgaa ccagatgtga tctatgcagg
2281 acatgacaac acaaaacctg acacctccag ttctttgctg acaagtctta atcaactagg
2341 cgagaggcaa cttctttcag tagtcaagtg gtctaaatca ttgccaggtt ttcgaaactt
2401 acatattgat gaccagataa ctctcattca gtattcttgg atgagcttaa tggtgtttgg
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2581 gcagatccca caggagtttg tcaagcttca agttagccaa gaagagttcc tctgtatgaa
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2701 ggagatgagg tcaagctaca ttagagagct catcaaggca attggtttga ggcaaaaagg
2761 agttgtgtcg agctcacagc gtttctatca acttacaaaa cttcttgata acttgcatga
2821 tcttgtcaaa caacttcatc tgtactgctt gaatacattt atccagtccc gggcactgag
2881 tgttgaattt ccagaaatga tgtctgaagt tattgctgca caattaccca agatattggc
2941 agggatggtg aaacccccttc tctttcataa
```

Fig. 21